

SEQUENCE LISTING

<110> Rhône-Poulenc Rorer

5 <120> Polypeptides capable of interacting with
oncogenic mutants of the p53 protein

<130> Sequences

<140>

10 <141>

<150> FR9812754

<151> 1998-10-12

15 <160> 33

<170> PatentIn Ver. 2.1

<210> 1

20 <211> 23

<212> DNA

<213> Artificial sequence

<220>

25 <223> Artificial sequence description: oligonucleotide

<400> 1
agatctgtat ggaggagccg cag

23

<210> 2

30 <211> 29

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<213> Artificial sequence

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<223> Artificial sequence description: 3'-393
oligonucleotide (p53)

<400> 2

agatcttcac agtctgagtc aggccttc

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<210> 3

<211> 15

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<213> Artificial sequence

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<220>

<223> Artificial sequence description: 3' H175
oligonucleotide

<400> 3

ggggcagtgc ctcac

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<210> 4

<211> 15

<212> DNA

20 <213> Artificial sequence

<220>

<223> Artificial sequence description: 3' W248
oligonucleotide

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<400> 4

gggcctccag ttcac

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<210> 5

<211> 15

30 <212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: 3' H273
oligonucleotide

<400> 5
acaaacatgc acctc

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<210> 6
<211> 15
<212> DNA
<213> Artificial sequence

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<220>
<223> Artificial sequence description: 3' G281
oligonucleotide

<400> 6
gcgcgcggcct ctcctc

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15

<210> 7
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<212> DNA
<213> Artificial sequence

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<220>
<223> Artificial sequence description: 5'-73
oligonucleotide

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<400> 7
agatctgtgt ggccctgca cca

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<212> DNA
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<220>
<221> CDS

<222> (1)..(885)

<220>

<223> Artificial sequence description: murine MBP1

5 C-term fragment

<400> 8

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Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp	
1 5 10 15	
ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg	96
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu	
20 25 30	
ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct	144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro	
35 40 45	
aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca	192
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro	
50 55 60	
tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt	240
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys	
65 70 75 80	
aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc	288
Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile	
85 90 95	
gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac	336
Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn	
100 105 110	
gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg	384
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu	
115 120 125	
gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac	432
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His	
130 135 140	
caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc	480
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg	
145 150 155 160	
tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac	528
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp	
165 170 175	
aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct	576
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro	
180 185 190	
tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg	624
Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val	
195 200 205	
cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc	672

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Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
 210                      215                      220

tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac    720
Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225                      230                      235                      240

att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca    768
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
                      245                      250                      255

gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg    816
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
                      260                      265                      270

aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc    864
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
                      275                      280                      285

ttt gtg gga gcc tat acc ttc tgaagacct cagggaaggg ccatgtgggg    915
Phe Val Gly Ala Tyr Thr Phe
                      290                      295

gcccttccc cctcccatag ctttaagcagc cccggggggc tagggatgac cgttctgctt 975

aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaaa                1021

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- <210> 9
 - <211> 295
 - <212> PRT
 - <213> Artificial sequence
 - <223> Artificial sequence description: murine MBP1
C-term fragment

<400> 9

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 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
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 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
 35 40 45
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
 50 55 60
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
 65 70 75 80
 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
 85 90 95
 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
 100 105 110
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
 115 120 125
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
 130 135 140
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
 145 150 155 160
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
 165 170 175
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
 180 185 190
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
 195 200 205
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
 210 215 220
 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
 225 230 235 240
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
 245 250 255
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
 260 265 270
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
 275 280 285
 Phe Val Gly Ala Tyr Thr Phe
 290 295

<210> 10
 <211> 39
 <212> DNA
 <213> Artificial sequence

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<220>
 <223> Artificial sequence description: 5' c-myc
 oligonucleotide

<400> 10
 gatccatgga gcagaagctg atctccgagg aggacctga

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10

<210> 11
 <211> 39
 <212> DNA
 <213> Artificial sequence

15

<220>
 <223> Artificial sequence description: 3' c-myc
 oligonucleotide
 <400> 11

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gatctcaggt cctcctcgga gatcagcttc tgcctcatg

39

<210> 12
 <211> 45
 <212> DNA
 <213> Artificial sequence

25

<220>
 <223> Artificial sequence description: 5' MCS
 oligonucleotide

30

<400> 12
 gatctcggtc gacctgcatg caattcccgg gtgcggccgc gagct

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<210> 13
 <211> 37

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<212> DNA

<213> Artificial sequence

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5 <223> Artificial sequence description: 3' MCS
oligonucleotide

<400> 13

cgcgggccgca cccgggaatt gcatgcaggt cgaccga

37

10 <210> 14

<211> 22

<212> DNA

<213> Artificial sequence

15 <220>

<223> Artificial sequence description: 3' mMBP1
oligonucleotide

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<210> 15

<211> 1513

<212> DNA

<213> Artificial sequence

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<221> CDS

<222> (49)..(1377)

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<223> Artificial sequence description: murine MBP1
(complete sequence)

<400> 15

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Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu	
5 10 15	
ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc	153
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser	
20 25 30 35	
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac	201
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His	
40 45 50	
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt	249
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly	
55 60 65	
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc	297
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg	
70 75 80	
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca	345
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro	
85 90 95	
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct	393
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro	
100 105 110 115	
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg	441
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu	
120 125 130	
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac	489
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr	
135 140 145	
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg	537
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val	
150 155 160	
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac	585
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn	
165 170 175	
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga	633
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly	
180 185 190 195	
cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc	681
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala	
200 205 210	
cca tgt gag cag cgc tgc ctc aac tcc tat ggg acc ttc ctg tgt cgc	729
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg	
215 220 225	
tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat	777
Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	

230	235	240	
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc			825
Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val			
245	250	255	
aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg			873
Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu			
260	265	270	275
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca			921
Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala			
	280	285	290
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac			969
His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr			
	295	300	305
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca			1017
Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser			
	310	315	320
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag			1065
Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln			
	325	330	335
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt			1113
Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser			
	340	345	350
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt			1161
Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly			
	360	365	370
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc			1209
Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe			
	375	380	385
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg			1257
Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg			
	390	395	400
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc			1305
Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr			
	405	410	415
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg			1353
Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr			
	420	425	430
			435
gtc ttt gtg gga gcc tat acc ttc tgaagacct cagggaaggg ccatgtgggg			1407
Val Phe Val Gly Ala Tyr Thr Phe			
	440		
gccccctccc cctcccatag cttaagcagc cccggggggc tagggatgac cgttctgctt			1467
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa			1513

- <210> 16
- <211> 443
- <212> PRT
- <213> Artificial sequence
- 5 <223> Artificial sequence description: murine MBP1
(complete sequence)

<400> 16

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			20					25					30		
Pro	Asp	Ser	Tyr	Thr	Glu	Cys	Thr	Asp	Gly	Tyr	Glu	Trp	Asp	Ala	Asp
		35					40					45			
Ser	Gln	His	Cys	Arg	Asp	Val	Asn	Glu	Cys	Leu	Thr	Ile	Pro	Glu	Ala
	50					55					60				
Cys	Lys	Gly	Glu	Met	Lys	Cys	Ile	Asn	His	Tyr	Gly	Gly	Tyr	Leu	Cys
65					70					75					80
Leu	Pro	Arg	Ser	Ala	Ala	Val	Ile	Ser	Asp	Leu	His	Gly	Glu	Gly	Pro
				85					90					95	
Pro	Pro	Pro	Ala	Ala	His	Ala	Gln	Gln	Pro	Asn	Pro	Cys	Pro	Gln	Gly
			100					105					110		
Tyr	Glu	Pro	Asp	Glu	Gln	Glu	Ser	Cys	Val	Asp	Val	Asp	Glu	Cys	Thr
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Gln	Ala	Leu	His	Asp	Cys	Arg	Pro	Ser	Gln	Asp	Cys	His	Asn	Leu	Pro
	130					135					140				
Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro
145					150					155				160	
Glu	Cys	Val	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Arg	Tyr	Cys	Gln	His	Arg
				165					170					175	
Cys	Val	Asn	Leu	Pro	Gly	Ser	Phe	Arg	Cys	Gln	Cys	Glu	Pro	Gly	Phe
		180					185						190		
Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp
		195				200						205			
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe
	210					215					220				
Leu	Cys	Arg	Cys	Asn	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser
225					230					235				240	
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			245						250					255	
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly
		260					265						270		

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
 275 280 285
 Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
 290 295 300
 Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val
 305 310 315 320
 Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
 325 330 335
 Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser
 340 345 350
 Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
 355 360 365
 Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln
 370 375 380
 Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
 385 390 395 400
 Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
 405 410 415
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 420 425 430
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
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<210> 17

<211> 21

5 <212> DNA

<213> Artificial sequence

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10 <223> Artificial sequence description: 3' hMBP1
oligonucleotide

<400> 17

ctccgctccg aggtgatggt c

21

<210> 18

15 <211> 21

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: 5' hMBP1
oligonucleotide

5

<400> 18

tgtagctact ccagctacct c

21

<210> 19

<211> 1122

10 <212> DNA

<213> Artificial sequence

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15 <223> Artificial sequence description: human MBP1 cDNA
(partial sequence)

<400> 19

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cttgggatca gcttctctc aggattctga agagcccgac agctacacgg aatgcacaga 180
tggctatgag tgggaccag acagccagca ctgccggat gtcaacgagt gtctgacct 240
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cagtgatatt gatgagtgt gctactccag ctacctctgt cagtaccgct gcgtcaacga 840
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<210> 20

20 <211> 684

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: human MBP1 cDNA
(partial sequence)

<400> 20

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tgtgagtctg gtgcgcacca gtgctccgag gcccaaacct gtgtcaactt ccatgggggc 180
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ttttacatta ggcaaataca caacgtcagc gccatgctgg tcttcgcccc gccggtgacg 480
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cgggccagct ctgtactgag gtcaccgtc ttgttagggg cctacacctt ctgaggagca 600
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<210> 21

<211> 1480

<212> DNA

10 <213> Artificial sequence

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<222> (59)..(1387)

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<223> Artificial sequence description: human MBP1
(complete sequence)

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Met	Leu	Pro	Cys	Ala	Ser	Cys	Leu	Pro	Gly	Ser	Leu	Leu	Leu	Trp	Ala	
1				5					10					15		
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Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Ala	Ser	Pro	Gln	Asp	Ser	Glu	Glu	
			20					25					30			
ccc	gac	agc	tac	acg	gaa	tgc	aca	gat	ggc	tat	gag	tgg	gac	cca	gac	202
Pro	Asp	Ser	Tyr	Thr	Glu	Cys	Thr	Asp	Gly	Tyr	Glu	Trp	Asp	Pro	Asp	
		35					40					45				
agc	cag	cac	tgc	cgg	gat	gtc	aac	gag	tgt	ctg	acc	atc	cct	gag	gcc	250
Ser	Gln	His	Cys	Arg	Asp	Val	Asn	Glu	Cys	Leu	Thr	Ile	Pro	Glu	Ala	
	50					55					60					
tgc	aag	ggg	gaa	atg	aag	tgc	atc	aac	cac	tac	ggg	ggc	tac	ttg	tgc	298
Cys	Lys	Gly	Glu	Met	Lys	Cys	Ile	Asn	His	Tyr	Gly	Gly	Tyr	Leu	Cys	
65					70					75				80		
ctg	ccc	cgc	tcc	gct	gcc	gtc	atc	aac	gac	cta	cac	ggc	gag	gga	ccc	346
Leu	Pro	Arg	Ser	Ala	Ala	Val	Ile	Asn	Asp	Leu	His	Gly	Glu	Gly	Pro	
				85					90					95		
cgg	cca	cca	gtg	cct	ccc	gct	caa	cac	ccc	aac	ccc	tgc	cca	cca	ggc	394
Pro	Pro	Pro	Val	Pro	Pro	Ala	Gln	His	Pro	Asn	Pro	Cys	Pro	Pro	Gly	
			100					105					110			
tat	gag	ccc	gac	gat	cag	gac	agc	tgt	gtg	gat	gtg	gac	gag	tgt	gcc	442
Tyr	Glu	Pro	Asp	Asp	Gln	Asp	Ser	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala	
		115					120					125				
cag	gcc	ctg	cac	gac	tgt	cgc	ccc	agc	cag	gac	tgc	cat	aac	ttg	cct	490
Gln	Ala	Leu	His	Asp	Cys	Arg	Pro	Ser	Gln	Asp	Cys	His	Asn	Leu	Pro	
	130					135					140					
ggc	tcc	tat	cag	tgc	acc	tgc	cct	gat	ggc	tac	cgc	aag	atc	ggg	ccc	538
Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro	
145				150					155					160		
gag	tgt	gtg	gac	ata	gac	gag	tgc	cgc	tac	cgc	tac	tgc	cag	cac	cgc	586
Glu	Cys	Val	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Arg	Tyr	Cys	Gln	His	Arg	
				165				170					175			
tgc	gtg	aac	ctg	cct	ggc	tcc	ttc	cgc	tgc	cag	tgc	gag	cgg	ggc	ttc	634

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe	
180 185 190	
cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac	682
Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp	
195 200 205	
atg ggg gcc cca tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc	730
Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe	
210 215 220	
ctg tgt cgc tgc cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc	778
Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser	
225 230 235 240	
tgc agt gat att gat gag tgt agc tac tcc agc tac ctc tgt cag tac	826
Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr	
245 250 255	
cgc tgc gtc aac gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt	874
Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly	
260 265 270	
tac cag ctg ctg gcc aca cgc ctc tgc caa gac att gat gag tgt gag	922
Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu	
275 280 285	
tct ggt gcg cac cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat	970
Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His	
290 295 300	
ggg ggc tac cgc tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc	1018
Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile	
305 310 315 320	
cag gtc tct gag aac cgc tgc ctc tgc ccg gcc tcc aac cct cta tgt	1066
Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys	
325 330 335	
cga gag cag cct tca tcc att gtg cac cgc tac atg acc atc acc tcg	1114
Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser	
340 345 350	
gag cgg agc gtg ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc	1162
Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val	
355 360 365	
tac ccc ggt gcc tac aat gcc ttt cag atc cgt gct gga aac tcg cag	1210
Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln	
370 375 380	
ggg gac ttt tac att agg caa atc aac aac gtc agc gcc atg ctg gtc	1258
Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val	
385 390 395 400	
ctc gcc cgg ccg gtg acg ggc ccc cgg gag tac gtg ctg gac ctg gag	1306
Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu	
405 410 415	

atg gtc acc atg aat tcc ctc atg agc tac cgg gcc agc tct gta ctg 1354
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
 420 425 430

agg ctc acc gtc ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca 1407
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
 435 440

ccctccctgc agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa 1467

taaagggaga aag 1480

- <210> 22
 5 <211> 443
 <212> PRT
 <213> Artificial sequence
 <273> Artificial sequence description: human MBP1
 (complete sequence)

<400> 22

Met	Leu	Pro	Cys	Ala	Ser	Cys	Leu	Pro	Gly	Ser	Leu	Leu	Leu	Trp	Ala
1				5					10					15	
Leu	Leu	Leu	Leu	Leu	Leu	Gly	Ser	Ala	Ser	Pro	Gln	Asp	Ser	Glu	Glu
			20					25					30		
Pro	Asp	Ser	Tyr	Thr	Glu	Cys	Thr	Asp	Gly	Tyr	Glu	Trp	Asp	Pro	Asp
		35					40					45			
Ser	Gln	His	Cys	Arg	Asp	Val	Asn	Glu	Cys	Leu	Thr	Ile	Pro	Glu	Ala
	50						55					60			
Cys	Lys	Gly	Glu	Met	Lys	Cys	Ile	Asn	His	Tyr	Gly	Gly	Tyr	Leu	Cys
	65				70					75					80
Leu	Pro	Arg	Ser	Ala	Ala	Val	Ile	Asn	Asp	Leu	His	Gly	Glu	Gly	Pro
				85					90					95	
Pro	Pro	Pro	Val	Pro	Pro	Ala	Gln	His	Pro	Asn	Pro	Cys	Pro	Pro	Gly
			100					105					110		
Tyr	Glu	Pro	Asp	Asp	Gln	Asp	Ser	Cys	Val	Asp	Val	Asp	Glu	Cys	Ala
		115					120						125		
Gln	Ala	Leu	His	Asp	Cys	Arg	Pro	Ser	Gln	Asp	Cys	His	Asn	Leu	Pro
	130					135						140			
Gly	Ser	Tyr	Gln	Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro
	145				150					155				160	
Glu	Cys	Val	Asp	Ile	Asp	Glu	Cys	Arg	Tyr	Arg	Tyr	Cys	Gln	His	Arg
			165						170					175	
Cys	Val	Asn	Leu	Pro	Gly	Ser	Phe	Arg	Cys	Gln	Cys	Glu	Pro	Gly	Phe
		180					185						190		
Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp
	195					200						205			

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
 210 215 220
 Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
 225 230 235 240
 Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr
 245 250 255
 Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
 260 265 270
 Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
 275 280 285
 Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
 290 295 300
 Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile
 305 310 315 320
 Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
 325 330 335
 Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser
 340 345 350
 Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
 355 360 365
 Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln
 370 375 380
 Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
 385 390 395 400
 Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
 405 410 415
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
 420 425 430
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
 435 440

<210> 23

5 <211> 817

<212> DNA

<213> Artificial sequence

<220>

<223> Artificial sequence description: murine MBP1
cDNA (partial sequence)

<400> 23
gctgtggcag aaaccctga cttctgccca ccaactccca gcctcaggat gctccctttt 60

gcctcctgcc tccccgggtc ttgtgtgtc tgggcgtttc tgctgttgct cttgggagca 120
gcgtcccccac aggatcccgga ggagccggac agctacacgg aatgcacaga tggctatgag 180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgacctat cccggaggct 240
tgcaaggggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gcctcgtctt 300
gctgccgtca tcagtgatct ccatgggtgaa ggacctccac cggcaggggc ccatgctcaa 360
caaccaaacc cttgcccgcga gggctacgag cctgatgaac aggagagctg tgtggatgtg 420
gacgagtgtg cccagggcttt gcatgactgt cggcctagt caggactgcca taaccttctt 480
ggctcctacc agtgcaactg cctgatgggt taccgaaaaa ttggaccgga atgtgtggac 540
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctctttt 600
cgatgccagt gtgagccagg cttccagttg ggacctaaaca accgctcttg tgtggatgtg 660
aatgagtgtg acatggggagc cccatgtgag cagcgtctgt tcaactccta tgggaccttc 720
ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctctctg cagcgatatc 780
gatgagtgcg gctactccag ttacctctgc cagtacc 817

5

<210> 24
<211> 24
<212> DNA
<213> Artificial sequence

10

<220>
<223> Artificial sequence description: sense-GAPDH
oligonucleotide

<400> 24
cggagtcaac ggatttgggc gtat 24

15

<210> 25
<211> 24
<212> DNA
20 <213> Artificial sequence

<220>
<223> Artificial sequence description: antisense-GAPDH
oligonucleotide

25

<400> 25
agccttctcc atgggtggga agac 24

<210> 26
 <211> 25
 <212> DNA
 <213> Artificial sequence

5

<220>
 <223> Artificial sequence description: oligonucleotide

<400> 26
 cgggtggcct tgggggttcag ggggg

25

10

<210> 27
 <211> 21
 <212> DNA
 <213> Artificial sequence

15

<220>
 <223> Artificial sequence description: sense MBP1
 oligonucleotide

<400> 27
 gccctgatgg ttaccgcaag a

21

20

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial sequence

25

<220>
 <223> Artificial sequence description: antisense MBP1
 oligonucleotide

30

<400> 28
 agcccccattg gaagttgaca c

21

<210> 29
 <211> 20

<212> DNA

<213> Artificial sequence

<220>

- 5 <223> Artificial sequence description: sense-actin
oligonucleotide

<400> 29

gtggggcgcc ccaggcacca

20

10 <210> 30

<211> 1358

<212> DNA

<213> Artificial sequence

15 <220>

<221> CDS

<222> (1)..(885)

<220>

- 20 <223> Artificial sequence description: human MBP1
C-term fragment

<400> 30

tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac	48
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp	
1 5 10 15	

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg	96
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu	
20 25 30	

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct	144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro	
35 40 45	

aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca	192
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro	
50 55 60	
tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc	240
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys	
65 70 75 80	
cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att	288
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile	
85 90 95	
gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac	336
Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn	
100 105 110	
gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt tac cag ctg ctg	384
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu	
115 120 125	
gcc aca cgc ctc tgc caa gac att gat gag tgt gag tct ggt gcg cac	432
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His	
130 135 140	
cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat ggg ggc tac cgc	480
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg	
145 150 155 160	
tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc cag gtc tct gag	528
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu	
165 170 175	
aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt cga gag cag cct	576
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro	
180 185 190	
tca tcc att gtg cac cgc tac atg acc atc acc tcc gag cgg agc gtg	624
Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val	
195 200 205	
ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc tac ccc ggt gcc	672
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala	
210 215 220	
tac aat gcc ttt cag atc cgt gct gga aac tcc cag ggg gac ttt tac	720
Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr	
225 230 235 240	
att agg caa atc aac aac gtc agc gcc atg ctg gtc ctc gcc cgg ccg	768
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro	
245 250 255	
gtg acg ggc ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg	816
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met	
260 265 270	
aat tcc ctc atg agc tac cgg gcc agc tct gta ctg agg ctc acc gtc	864
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val	

275

280

285

ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca ccctccctgc 915
 Phe Val Gly Ala Tyr Thr Phe
 290 295

agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa taaagggaga 975
 aagaaagtcc tggtaggctga ggtggggcggg tcacactgca ggaagcctca ggctggggca 1035
 gggtaggcact tggggggggca ggccaagtgc acctaaatgg gggctctctat atgttcaggc 1095
 ccagggggccc ccattgacag gagctgggag ctctgcacca cgagcttcag tcaccccgag 1155
 aggagaggag gtaacgagga gggcggactc caggcccccgg cccagagatt tggacttggc 1215
 tggcttgtag gggctcctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca 1275
 ttcctaactc tgcctcaaac tgtacatttg gataagccct agtagttccc tgggcctgtt 1335
 tttctataaa acgaggcaac tgg 1358

<210> 31

<211> 295

5 <212> PRT

<213> Artificial sequence

<223> Artificial sequence description: human MBP1
 C-term fragment

<400> 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
 1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
 20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
 35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
 50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
 65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
 85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
 100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
 115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
 130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg

145	150	155	160
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu			
165	170	175	
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro			
180	185	190	
Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val			
195	200	205	
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala			
210	215	220	
Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr			
225	230	235	240
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro			
245	250	255	
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met			
260	265	270	
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val			
275	280	285	
Phe Val Gly Ala Tyr Thr Phe			
290	295		

<210> 32

<211> 1663

<212> DNA

5 <213> Artificial sequence

<220>

<221> CDS

<222> (1)..(999)

10

<220>

<223> Artificial sequence description: murine fibulin
2 c-term fragment

<400> 32

gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat 48
 Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
 1 5 10 15

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc 96
 Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
 20 25 30

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc 144
 Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
 35 40 45

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac 192
 Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His

gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat
 Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
 1 5 10 15

50	55	60	
aca tgt gag aac aca ccg ggc tcc tac cgc tgc tcc tgc gct gct ggc			240
Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly			
65	70	75	80
ttc ctt ttg gcc gca gat ggc aaa cat tgt gaa gat gtg aac gag tgc			288
Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys			
	85	90	95
gag act cgg cgc tgc agc cag gaa tgt gcc aac atc tat ggc tcc tat			336
Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr			
	100	105	110
cag tgc tac tgc cgt cag ggc tac cag ctg gca gag gat ggg cat acc			384
Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr			
	115	120	125
tgc aca gac atc gat gag tgt gca cag ggc gcg ggc att ctc tgt acc			432
Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr			
130	135	140	
ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag			480
Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu			
145	150	155	160
caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat			528
Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp			
	165	170	175
gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac			576
Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His			
	180	185	190
aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac			624
Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn			
	195	200	205
tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat			672
Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp			
210	215	220	
atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc			720
Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu			
225	230	235	240
aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc			768
Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly			
	245	250	255
cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag			816
Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys			
	260	265	270
ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act			864
Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr			
275	280	285	
ggg gtg gta tcc ctg cag cgg tct gtt ctg gag ccg cgg gac ttt gcc			912

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
 290 295 300

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
 305 310 315 320

ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca 1009
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro
 325 330

tgtcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tccaaagtgg 1069
 ctttttgctg tgactctgta acttaactta atcatgctga gctgggtggg cttgagcttc 1129
 taccctagag ggagggagat gcacccctagc aggcactgag tacaggccag ggtcaccctga 1189
 ggctagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc 1249
 aactatggct acagctgaca ttccattcct tcatccactg tgttccctcaa ttaaaaaaaaa 1309
 aaatcagctg tgcattgtag cacagacctt taatccctagc actggggagg cagaggtagg 1369
 tagatctctg agttccagge cagcctgggc tacactggga gttctaacca gccagagcta 1429
 catagagaga ccttatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc 1489
 agcctgggtct acgctgggag ttctaaccag ccagagctac atagagagat cctatctcaa 1549
 caaggaaaaa tgaaagaaat cattttaaaaa ggtttttttt ttgctgttg ttgtttaatg 1609
 ataagagtag cacatatata ttattaaaaa tgatcaaata gcacagaaag gtta 1663

<210> 33

<211> 333

5 <212> PRT

<213> Artificial sequence

<223> Artificial sequence description: murine fibulin
 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
 1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
 20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
 65 70 75 80

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
 85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
 100 105 110
 Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
 115 120 125
 Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
 130 135 140
 Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu
 145 150 155 160
 Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp
 165 170 175
 Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His
 180 185 190
 Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn
 195 200 205
 Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp
 210 215 220
 Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu
 225 230 235 240
 Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly
 245 250 255
 Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys
 260 265 270
 Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr
 275 280 285
 Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
 290 295 300
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
 305 310 315 320
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro
 325 330